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## RAW SEQUENCE LISTING

DATE: 08/27/2004

PATENT APPLICATION: US/10/734,149

TIME: 16:53:27

Input Set : N:\Crf3\RULE60\10734149.raw

Output Set: N:\CRF4\08272004\J734149.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: JULIUS, Michael H.; FILIPP, Dominik;  
 6 ALIZADEH-KHIAVI, Kamel  
 8 (ii) TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC  
 9 PROTEIN (CD14), ENCODING GENE AND APPLICATION  
 10 IN B CELL ACTIVATION

12 (iii) NUMBER OF SEQUENCES: 15

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Blake, Cassels & Graydon  
 16 (B) STREET: Box 25, Commerce Court West  
 17 (C) CITY: Toronto  
 18 (D) STATE: Ontario  
 19 (E) COUNTRY: Canada  
 20 (F) ZIP: M5L 1A9

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
 24 (B) COMPUTER: COMPAQ, IBM PC compatible  
 25 (C) OPERATING SYSTEM: MS-DOS 5.1  
 26 (D) SOFTWARE: WORD PERFECT

28 (vi) CURRENT APPLICATION DATA:

29 (A) APPLICATION NUMBER: US/10/734,149  
 30 (B) FILING DATE: 15-Dec-2003

34 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/09/313,177  
 33 (B) FILING DATE: 18-May-1999  
 35 (A) APPLICATION NUMBER: 08/746,883  
 36 (B) FILING DATE: November 18, 1996  
 38 (A) APPLICATION NUMBER: PCT/CA 97/00880  
 39 (B) FILING DATE: November 18, 1997

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Hunt, John C.  
 43 (B) REGISTRATION NUMBER: 36,424  
 44 (C) REFERENCE/DOCKET NUMBER: 47841/00047

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: (416) 863-4344  
 48 (B) TELEFAX: (416) 863-2653

## 51 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 1122 base pairs  
 54 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: single  
 56 (D) TOPOLOGY: linear

ENTERED

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57      (ii) MOLECULE TYPE: cDNA
59      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 ATGGTGTGCG TGCCCTACCT GCTGCTGCTG CTGCTGCCGT CACTGCTGCG TGTGTCTGCG      60
63 GACACAACAG AACCTGCGA GCTGGACGAC GACGATTTC GTTGTGTCTG CAACTTCACG      120
65 GATCCGAAGC CTGACTGGTC TAGCGCCGTT CAGTGTATGG TTGCCGTCGA GGTGGAGATC      180
67 AGTGCCGGCG GCCGCAGCCT GGAACAGTTT CTCAAGGGAG CCGACACCAA CCCGAAGCAG      240
69 TATGCTGACA CAATCAAGGC TCTGCGCGTT CGGCGACTCA AGCTGGGCGC TGCACAGGTT      300
71 CCTGCTCAGC TTCTGGTCGC CGTTCTGCGC GCGCTCGGGT ACTCTCGTCT CAAGGAACTG      360
73 ACGCTTGAGG ACCTGGAGGT AACCGGCCCA ACGCCCCCGA CGCCTCTGGA AGCCGCTGGG      420
75 CCTGCGCTCA CCACCCTCAG TCTGCGTAAC GTATCGTGGA CAACAGGAGG TGCCTGGCTC      480
77 GGCGAACTGC AGCAGTGGCT CAAGCCTGGG CTCAGGGTGC TGAACATTGC CCAAGCACAC      540
79 TCGCTTGCCCT TTCCGTGCGC AGGGCTCTCC ACCTTCGAGG CGCTCACCAC CCTAGACCTG      600
81 TCTGACAATC CCAGTCTCGG CGACACGGGG CTGATGGCAG CTCTCTGTCC GAACAAGTTC      660
83 CCGGCCCTCC AATATCTAGC GCTACGCAAC GCGGGGATGG AGACGCCGAG CGGCGTGTGC      720
85 GCGGCGCTGG CCGCAGCGAG GGTGCAGCCC CAAAGCCTGG ACCTCAGCCA CAACTCGCTG      780
87 CGCGTCACCG CCCCGGGTGC TACCCGATGT GTCTGGCCCC GTGACTAAG GTCTCTCAAT      840
89 TTGTCGTTTC CTGGGCTGGA GCAAGTGCCCT AAGGGACTGC CCCCTAAGCT CAGCGTGCTT      900
91 GATCTCAGCT GCAACAAGCT AAGCAGGGAG CCGCGGCGAG ACGAGCTGCC CGAGGTAAAT      960
93 GACCTGACTC TGGACGAAA TCCCTTTCTG GACCCTGGAG CCCTCCAGCA CCAAATGAC      1020
95 CCGATGATCT CCGGCGTGGT CCCAGCCTGT GCGCGTTCTG CCTTGACCAT GGGGGTGTC      1080
97 GGAGCCCTGG CGCTGCTTCA AGGAGCCCGA GGCTTCGCGT AA      1122
100 (2) INFORMATION FOR SEQ ID NO: 2:
101      (i) SEQUENCE CHARACTERISTICS:
102          (A) LENGTH: 1128 base pairs
103          (B) TYPE: nucleic acid
104          (C) STRANDEDNESS: single
105          (D) TOPOLOGY: linear
106      (ii) MOLECULE TYPE: cDNA
108      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
110 ATGGAGCGCG CGTCTGCTT GTTGCTGCTG CTGCTGCCGC TGGTGACGCT CTCTGCGACC      60
112 ACGCCAGAAC CTTGTGAGCT GGACGATGAA GATTTCGCT CCGTCTGCAA CTCTCCGAA      120
114 CCTCAGCCCG ACTGGTCCGA AGCCTTCCAG TGTGTGTCTG CAGTAGAGGT GGAGATCCAT      180
116 GCCGGCGGTC TCAACCTAGA GCCGTTTCTA AAGCGGCTCG ATGCGGACGC CGACCCGCGG      240
118 CAGTATGCTG ACACGGTCAA GGCTCTCCGC GTGCGGCGGC TCACAGTGGG AGCCGCACAG      300
120 GTTCCTGCTC AGCTACTGGT AGGCGCCCTG CGTGTGCTAG CGTACTCCCG CCTCAAGGAA      360
122 CTGACGCTCG AGGACCTAAA GATAACCGGC ACCATGCCTC CGCTGCCTCT GGAAGCCACA      420
124 GGAATTGCAC TTTCCAGCTT GCGCCTACGC AACGTGTCGT GGGCGACAGG GCGTTCTTGG      480
126 CTCGCCGAGC TGCAGCAGTG GCTCAAGCCA GGCCTCAAGG TACTGAGCAT TGCCCAAGCA      540
128 CACTCGCCTG CCTTTTCCTG CGAACAGGTT CGCGCCTTCC CGGCCCTTAC CAGCCTAGAC      600
130 CTGTCTGACA ATCCTGGACT GGGCGAACGC GGACTGATGG CGGCTCTCTG TCCCCACAAG      660
132 TTCCCGGCCA TCCAGAATCT AGCGCTGCGC AACACAGGAA TGGAGACGCC CACAGGCGTG      720
134 TGCGCCGCAC TGGCGGCGGC AGGTGTGCAG CCCACAGCC TAGACCTCAG CCACAACCTG      780
136 CTGCGCGCCA CCGTAAACCC TAGCGCTCCG AGATGCATGT GGTCCAGCGC CCTGAACTCC      840
138 CTCAATCTGT CGTTCGCTGG GCTGGAACAG GTGCCATAAG GACTGCCAGC CAAGCTCAGA      900
140 GTGCTCGATC TCAGCTGCAA CAGACTGAAC AGGCGGCCGC AGCCTGACGA GCTGCCCCGAG      960
142 GTGGATAACC TGACACTGGA CGGGAATCCC TTCTGGTCC CTGGAAGTGC CCTCCCCAC      1020
144 GAGGGCTCAA TGAATCCGG CGTGGTCCCA GCCTGTGCAC GTTCGACCTT GTCGGTGGGG      1080
146 GTGTCGGGAA CCCTGGTGCT GTCCAAGGG GCCCGGGGCT TTGCCTAA      1128
149 (2) INFORMATION FOR SEQ ID NO: 3:

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Input Set : N:\Cr3\RULE60\10734149.raw

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150      (i) SEQUENCE CHARACTERISTICS:
151          (A) LENGTH: 1101 base pairs
152          (B) TYPE: nucleic acid
153          (C) STRANDEDNESS: single
154          (D) TOPOLOGY: linear
155      (ii) MOLECULE TYPE: cDNA
156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
159 ATGGAGCGTG TGCTTGGCTT GTTGCTGTTG CTTCTGGTGC ACGCCTCTCC CGCCCCACCA      60
161 GAGCCCTGCG AGCTAGACGA GGAAAGTTGT TCCTGCAACT TCTCAGATCC GAAGCCAGAT      120
163 TGGTCCAGCG CTTTCAATTG TTTGGGGGCG GCAGATGTGG AATTGTACGG CGGCGGCCGC      180
165 AGCCTGGAAT ACCTTCTAAA GCGTGTGGAC ACGGAAGCAG ATCTGGGGCA GTTCACTGAT      240
167 ATTATCAAGT CTCTGTCCTT AAAGCGGCTT ACGGTGCGGG CCGCGCGGAT TCCTAGTCGG      300
169 ATTCTATTCG GAGCCCTGCG TGTGCTCGGG ATTTCCGGCC TCCAGGAACT GACTCTTGAA      360
171 AATCTCGAGG TAACCGGCAC CGCGCCGCCA CCGCTTCTGG AAGCCACCGG ACCCGATCTC      420
173 AACATCTTGA ACCTCCGCAA CGTGTCTGTT GCAACAAGGG ATGCCTGGCT CGCAGAACTG      480
175 CAGCAGTGGC TAAAGCCTGG ACTCAAGGTA CTGAGTATTG CCCAAGCACA CTCACTCAAC      540
177 TTTTCTGCG AACAGGTCCG CGTCTTCCCT GCCCTCTCCA CCTTAGACCT GTCTGACAAT      600
179 CCTGAATTGG GCGAGAGAGG ACTGATCTCA GCCCTCTGTC CCCTCAAGTT CCCGACCCTC      660
181 CAAGTTTTAG CGCTGCGTAA CGCGGGGATG GAGACGCCCA GCGGCGTGTG CTCTGCGCTG      720
183 GCCGCAGCAA GGGTACAGCT GCAAGGACTA GACCTTAGTC ACAATTCACT GCGGGATGCT      780
185 GCAGGCGCTC CGAGTTGTGA CTGGCCAGT CAGCTAAACT CGCTCAATCT GTCTTTCCT      840
187 GGGCTGAAGC AGGTACCTAA AGGGCTGCCA GCCAAGCTCA GCGTGCTGGA TCTCAGTTAC      900
189 AACAGGCTGG ATAGGAACCC TAGCCCAGAT GAGCTGCCCC AAGTGGGGAA CCTGTCACTT      960
191 AAAGGAAATC CTTTTTTGGA CTCTGAATCC CACTCGGAGA AGTTTAACTC TGGCGTAGTC      1020
193 ACCGCCGAG CTCCATCATC CCAAGCAGTG GCCTTGTCAG GAACTCTGGC TTTGCTCCTA      1080
195 GGAGATCGCC TCTTTGTTTA A                                1101

198 (2) INFORMATION FOR SEQ ID NO: 4:
199      (i) SEQUENCE CHARACTERISTICS:
200          (A) LENGTH: 373 amino acids
201          (B) TYPE: amino acid
202          (C) STRANDEDNESS:
203          (D) TOPOLOGY: linear
204      (ii) MOLECULE TYPE: protein
205      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
208 Met Val Cys Val Pro Tyr Leu Leu Leu Leu Leu Leu Pro Ser Leu Leu
209      1          5          10          15
211 Arg Val Ser Ala Asp Thr Thr Glu Pro Cys Glu Leu Asp Asp Asp Asp
212      20          25          30
214 Phe Arg Cys Val Cys Asn Phe Thr Asp Pro Lys Pro Asp Trp Ser Ser
215      35          40          45
217 Ala Val Gln Cys Met Val Ala Val Glu Val Glu Ile Ser Ala Gly Gly
218      50          55          60
220 Arg Ser Leu Glu Gln Phe Leu Lys Gly Ala Asp Thr Asn Pro Lys Gln
221      65          70          75          80
223 Tyr Ala Asp Thr Ile Lys Ala Leu Arg Val Arg Arg Leu Lys Leu Gly
224      85          90          95
226 Ala Ala Gln Val Pro Ala Gln Leu Leu Val Ala Val Leu Arg Ala Leu
227      100         105         110
229 Gly Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Glu Val Thr

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230          115          120          125
232 Gly Pro Thr Pro Pro Thr Pro Leu Glu Ala Ala Gly Pro Ala Leu Thr
233          130          135          140
235 Thr Leu Ser Leu Arg Asn Val Ser Trp Thr Thr Gly Gly Ala Trp Leu
236          145          150          155          160
238 Gly Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Arg Val Leu Asn Ile
239          165          170          175
241 Ala Gln Ala His Ser Leu Ala Phe Pro Cys Ala Gly Leu Ser Thr Phe
242          180          185          190
244 Glu Ala Leu Thr Thr Leu Asp Leu Ser Asp Asn Pro Ser Leu Gly Asp
245          195          200          205
247 Thr Gly Leu Met Ala Ala Leu Cys Pro Asn Lys Phe Pro Ala Leu Gln
248          210          215          220
250 Tyr Leu Ala Leu Arg Asn Ala Gly Met Glu Thr Pro Ser Gly Val Cys
251          225          230          235          240
253 Ala Ala Leu Ala Ala Arg Val Gln Pro Gln Ser Leu Asp Leu Ser
254          245          250          255
256 His Asn Ser Leu Arg Val Thr Ala Pro Gly Ala Thr Arg Cys Val Trp
257          260          265          270
259 Pro Ser Ala Leu Arg Ser Leu Asn Leu Ser Phe Ala Gly Leu Glu Gln
260          275          280          285
262 Val Pro Lys Gly Leu Pro Pro Lys Leu Ser Val Leu Asp Leu Ser Cys
263          290          295          300
265 Asn Lys Leu Ser Arg Glu Pro Arg Arg Asp Glu Leu Pro Glu Val Asn
266          305          310          315          320
268 Asp Leu Thr Leu Asp Gly Asn Pro Phe Leu Asp Pro Gly Ala Leu Gln
269          325          330          335
271 His Gln Asn Asp Pro Met Ile Ser Gly Val Val Pro Ala Cys Ala Arg
272          340          345          350
274 Ser Ala Leu Thr Met Gly Val Ser Gly Ala Leu Ala Leu Leu Gln Gly
275          355          360          365
277 Ala Arg Gly Phe Ala
278          370

```

281 (2) INFORMATION FOR SEQ ID NO: 5:

282 (i) SEQUENCE CHARACTERISTICS:

283 (A) LENGTH: 375 amino acids

284 (B) TYPE: amino acid

285 (C) STRANDEDNESS:

286 (D) TOPOLOGY: linear

287 (ii) MOLECULE TYPE: protein

289 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

291 Met Glu Arg Ala Ser Cys Leu Leu Leu Leu Leu Leu Pro Leu Val His
292 1          5          10          15
294 Val Ser Ala Thr Thr Pro Glu Pro Cys Glu Leu Asp Asp Glu Asp Phe
295          20          25          30
297 Arg Cys Val Cys Asn Phe Ser Glu Pro Gln Pro Asp Trp Ser Glu Ala
298          35          40          45
300 Phe Gln Cys Val Ser Ala Val Glu Val Glu Ile His Ala Gly Gly Leu
301          50          55          60

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```

303 Asn Leu Glu Pro Phe Leu Lys Arg Val Asp Ala Asp Ala Asp Pro Arg
304 65 70 75 80
306 Gln Tyr Ala Asp Thr Val Lys Ala Leu Arg Val Arg Arg Leu Thr Val
307 85 90 95
309 Gly Ala Ala Gln Val Pro Ala Gln Leu Leu Val Gly Ala Leu Arg Val
310 100 105 110
312 Leu Ala Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Lys Ile
313 115 120 125
315 Thr Gly Thr Met Pro Pro Leu Pro Leu Glu Ala Thr Gly Leu Ala Leu
316 130 135 140
318 Ser Ser Leu Arg Leu Arg Asn Val Ser Trp Ala Thr Gly Arg Ser Trp
319 145 150 155 160
321 Leu Ala Glu Leu Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser
322 165 170 175
324 Ile Ala Gln Ala His Ser Pro Ala Phe Ser Tyr Glu Gln Val Arg Ala
325 180 185 190
327 Phe Pro Ala Leu Thr Ser Leu Asp Leu Ser Asp Asn Pro Gly Leu Gly
328 195 200 205
330 Glu Arg Gly Leu Met Ala Ala Leu Cys Pro His Lys Phe Pro Ala Ile
331 210 215 220
333 Gln Asn Leu Ala Leu Arg Asn Thr Gly Met Glu Thr Pro Thr Gly Val
334 225 230 235 240
336 Cys Ala Ala Leu Ala Ala Ala Gly Val Gln Pro His Ser Leu Asp Leu
337 245 250 255
339 Ser His Asn Ser Leu Arg Ala Thr Val Asn Pro Ser Ala Pro Arg Cys
340 260 265 270
342 Met Trp Ser Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Ala Gly Leu
343 275 280 285
345 Glu Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Arg Val Leu Asp Leu
346 290 295 300
348 Ser Cys Asn Arg Leu Asn Arg Ala Pro Gln Pro Asp Glu Leu Pro Glu
349 305 310 315 320
351 Val Asp Asn Leu Thr Leu Asp Gly Asn Pro Phe Leu Val Pro Gly Thr
352 325 330 335
354 Ala Leu Pro His Glu Gly Ser Met Asn Ser Gly Val Val Pro Ala Cys
355 340 345 350
357 Ala Arg Ser Thr Leu Ser Val Gly Val Ser Gly Thr Leu Val Leu Leu
358 355 360 365
360 Gln Gly Ala Arg Gly Phe Ala
361 370 375

```

364 (2) INFORMATION FOR SEQ ID NO: 6:

365 (i) SEQUENCE CHARACTERISTICS:

366 (A) LENGTH: 366 amino acids

367 (B) TYPE: amino acid

368 (C) STRANDEDNESS:

369 (D) TOPOLOGY: linear

370 (ii) MOLECULE TYPE: protein

372 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

374 Met Glu Arg Val Leu Gly Leu Leu Leu Leu Leu Val His Ala Ser

**VERIFICATION SUMMARY**

PATENT APPLICATION: **US/10/734,149**

DATE: 08/27/2004

TIME: 16:53:28

Input Set : **N:\Crf3\RULE60\10734149.raw**

Output Set: **N:\CRF4\08272004\J734149.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:34 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:38 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)  
L:41 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]  
L:46 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]